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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
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Gapop 10.0 , Gapext 0.5
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1623
1 MMYDDNGNESSATYFILIGL......KEIRQRILRLFHVATHASEP 318
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        Issued_Patents_AA:*
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/backfiles1.pep:*
   US-09-605-785-527
US-09-439-313-527
US-09-439-313-527
US-09-053-303-2
US-09-053-303-2
US-09-053-303-2
US-09-339-115-2
PCT-US-98-876-5
US-08-98-876-5
US-08-467-947A-2
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US-08-465-947A-2
US-08-339-115-3
PCT-US93-0339-115-3
PCT-US93-07093-3
US-08-748-506-24
US-08-748-506-12
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Sequence 3, Appli
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Sequence 20, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 11, Appl
Sequence 67, Appl
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318	.318	318.5	318.5	320	320	326	326	329	329	330	332.5	332.5	333	335.5	335.5	336.5	336.5
19.6	19.6	19.6	19.6	19.7	19.7	20.1	20.1	20.3	20.3	20.3	20.5	20.5	20.5	20.7	20.7	20.7	20.7
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PCT-US93-08528-63	US-08-118-270-63	PCT-US93-08528-66	US-08-118-270-66	PCT-US93-08528-69	US-08-118-270-69	PCT-US93-08528-65	US-08-118-270-65	PCT-US93-08528-68	US-08-118-270-68	US-08-748-506-19	US-08-748-506-23	US-08-748-506-22	US-08-748-506-11	PCT-US93-08528-62	US-08-118-270-62	PCT-US93-08528-60	US-08-118-270-60
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App1	App1	Appl	App1	App1	App1	App1	Appl	Appl	App1	Appl	Appl	Appl	Appl	App1	Appl	App1	Appl

# ALIGNMENTS

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Qy 128 AICHPLRHATVLTLPRVTKIGVA            	QY 68 MLSGIDILISTSSMPKMLAIFWFNS   :  ::   :   :  :  :    Db 64 MLAAIDLALSTSTMPKILALFWFDS	Qy 8 NESSATYFILIGLPGLEEAQFWLAFPL   :     :   :   :     :     Db 5 NFTHAT-FVLIGIPGLEKAHFWVGFPL	Query Match 60.6%; Best Local Similarity 59.8%; Matches 183; Conservative 5	; ORGANISM: Homo sapiens US-09-605-785-527	; LENGTH: 320 ; TYPE: PRT	stSEQ for Windows	; NUMBER OF SEQ ID NOS: 835	APPLICATION NU	INVENTION: ERENCE: 21012	; TITLE OF INVENTION: COMPOSITIO	Skeiky,	; APPLICANT: L1, Samuel ; APPLICANT: Wang, Aijun	: Carter, Darrick	; APPLICANT: Day, Craig H. ; APPLICANT: Vedvick, Thomas S.	stolk, John	; APPLICANT: Fanger, Gary R.	: Kalos,	Henderson, Robert	٠. ٠	; APPLICANT: Mitcham, Jenniler L. : APPLICANT: Harlocker, Susan L.	••	••	=	; Patent No. 6321716	605-	RESULT 1
AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 187             :  :     :  :	MLSGIDILISTSSMPKHLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLANAFDRYV 127   :  :  :   :   :        :          :  :	NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFIC 67   :     :   :   :     :      : :: :    :::	Score 983; DB 4; Length 320; Pred. No. 8.9e-83; 54; Mismatches 67; Indels 2; Gaps 2;			Version 3.0	-2)	5/09/605,785	DIAGNOSIS OF PROSTATE CANCER 1.427C16	WILLIAM COMPOSITIONS AND METHODS FOR THE THERAPY AND	• ·							Α.		T.				900700	000708	

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US-09-439-313-527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 527
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TILE REFERENCE: 210121.427C9
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                                                                                                                                          MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH
                                                                                                                                                                                     AICHPLRHAAVLNNTVTAQIGIVAVVRGSLFFFFLPLLIKRLAFCHSNVLSHSYCVHQDV 183
                                                                                                                                                                                                     AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV
                                                                                                                                                                                                                                                                  MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDRYV 127
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                               RLFHVA 312
                                                                                       VCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRIL 306
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AMFKIS 309
                                                           IGVVLAFYVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVL
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Fanger, Gary
Retter, Mark
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; Pred. No. 8.9e-83;
54; Mismatches 67;
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 320;
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RESULT

US-09-053-303-2

Sequence 2, Application US/09053303
Patent No. 5948890
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-465-980-2
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                               Matches 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 320 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                       192 LPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAFY 251
                                                                                                                                                 136 ATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI 195
252 VPLIGLSVYHREGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVLAMEKIS 309
                                                                                             196 RVNVYYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIFY 254
                                                                                                                                                                                                                        72 LSTSTMPKILALFWFDSREISIEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 06-JUI CLASSIFICATION: 53
                                                                                                                                                                                                                                              76 ISTSSMPKMLAIFWFNSTTIQEDACLLQMFAIHSLSGMESTVLLAMAFDRYVAICHPLRH 135
                                                                                                                                                                                                                                                                                                      12 VLIGIPGLEKAHFWYGFPLLSMYVVAMCGNCIVVFIVRTERSLHAPMYLFLCMLAAIDLA 71
                                                                                                                                                                                                                                                                                                                                        16 ILIGLPGLEEAQEWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Roseland
STATE: New Jersey
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                                   VPFIGLSMYHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 312
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E: STUART & OLSTEIN
6 Becker Farm Road
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Li, Yi
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59.7%;
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Pred. No. 1.9e-81;
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Ruben, Steven

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                                                                                                   US-09-339-115-2
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US-09-053-303-2
                                                                Sequence 2, Application Patent No. 6372891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                              GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                APPLICANT:
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PRIOR APPLICATION DATA:
APPLICANT:
                                                                                                                                                                                                                                                                                                              132
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                                                                                                                                                                                                                                                        196 RVNVYYGLIVIISAIGLDSLLISFSYLLILKTYLGL-TREAQAKAFGTCVSHVCAVFIFY 254
                                                                                                                                                                                    255 VPFIGLSMVHRESKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 312
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                                                                                                                                                                                                                                                                                                                                                136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                ATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI 195
                                                                                                                                                                   VPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309
                                                                                                                                                                                                                                                                                                          AAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADT 191
                                                                                                                                                                                                                                                                                                                                                                                                             ISTSSMPKMLAIEWENSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDRYVAICHPLRH 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178;
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            Soppet, Daniel R.
Li, Yi
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Rosen, Craig A.
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                                                                               US/09339115
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RESULT 6
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7 MOLECULE TYPE: protein
US-09-339-115-2
                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 178;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                 APPLICANT:
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              APPLICANT: Ruben, TITLE OF INVENTION:
                                             APPLICANT:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                   136 ATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI 195
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                                                                                                                                                                                                                                                                          192 LPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAFY 251
                                                                                                                                                                                                                                                                                                             196 RVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIFY 254
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                                                                                                                                                                                                                                                                                                                                                                                                                  72 LSTSTMPKILALFWFDSREISIEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLRH 131
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New Jersey
                                                                                                                  Application PC/TUS9507093
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amino acid
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                             Rosen, Craig A. Ruben, Steven M.
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                                                                               Soppet, Daniel
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HUMAN G-PROTEIN RECEPTOR HPRAJ70
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59.7%;
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RESULT 7
US-08-988-876-7
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                                                                                                                                                                                  Sequence 7, Application US/08988876 Patent No. 6063596
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Best Local Similarity
Matches 178; Conserv
                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                          APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                  TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED TITLE OF INVENTION: WITH IMMUNE RESPONSE
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CORRESPONDENCE ADDRESS:
                     NUMBER OF
                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                         196 RVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIFY 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 LSTSTMPKILALFWFDSREISIEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLRH 131
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New Jersey
                   SEQUENCES:
                                                                                               Lal, Preeti
Bandman, Olga
Hillman, Jennifer L.
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Pred. No. 1.9e-81;
3; Mismatches 66;
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                                                                                      US-08-988-876-5
                                                                                                    RESULT 8
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                                                Sequence 5, Applic Patent No. 6063596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                  GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
 APPLICANT:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                           185 QDVMKLACDDIRVN-----VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAK 238
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STREET: 3174 Port
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                      125 AÇCFPL-HYTAIMSPMLCLALVALSWVLTTFHAMLHTL--LMARLCFCADNVIPHFFCDM 181
                                                                                                                                                                                                                                                                                        182 SALLKLAFSDTRVNEWVIFIMGGLILVI-----PFLLILGSYARIVSSILKVPSSRGICK
                                                                                                                                                    294 NRDMKGALSRVIH 306
                                                                                                                                                                                     298 TKEIRORILRLFH 310
                                                                                                                                                                                                                                                     239 AFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPL-PVILANIYLLVPPVLNPIVYGVK 297
                                                                                                                                                                                                                                                                                                                                                                                     128 AICHPLRHATVLTLPRVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLH 184
                                                                                                                                                                                                                                                                                                                                                                                                                        65 NLSFSDLCFSSVTIPKLLQNMQNQDPSIPYADCLTQMYFFLLFGDLESFLLVAMAYDRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                           68 MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDRYV
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3174 Porter Drive
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Lal, Pree
Bandman,
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34.8%; Pred. No. 3.8
tive 63; Mismatches
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RESULT 9
US-08-988-876-6
; Sequence 6, Application US/08988876
; Patent No. 6063596
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GENERAL INFORMATION:
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LIBRARY: GenBank
CLONE: 1314667
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LENGTH: 309 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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PRIOR APPLICATION DATA:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                       245
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                                                                                                                                                                                    125 AICYPLHYMVIMNPQLCSLLLLVSWIMSALHSLLQTLMVLRLSFCTHFQIPHFFCELNQM 184
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                                                                                                                                                                                                                                                                                                                                                         SHLSVVSLFYCTSLGVYLSSAAPQSTHTSS-
                                                                                                                                                                   IQLACSDTFLNNMMLYFAAILLGVAPLVGVL--YSYFKIVSSIRGISSAHSKYKAFSTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                          88;
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3174 Porter Drive
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Pred. No. 4e-29;
5; Mismatches 1
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Best Local Similarity
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CLONE: 205814
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LENGTH: 333 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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APPLICATION NUMBER:
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TITLE OF INVENTION: G PROTEIN COUPLED REV
TITLE OF INVENTION: WITH IMMUNE RESPONSE
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294 NKDVKSVLKKTLCEEVIRSPPSLLHFFLVLCH
                                                                                                      239 AFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANI-YLLVPPVLNPIVYGVK 297
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                                    298 TKEIRQ----
                                                                                                                                                                                  182 CLHQDVMKLACDDIRVN--VVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTR-EAQAK 238
                                                                                                                                                                                                                       123 YVAICHPMHYTVIMNYKLCGFLVLVSWIVSVLH--ALFQSL--MMLALPFCTHLEIPHYF 178
                                                                                                                                                                                                                                                                                                63 LSNLSEVDICFISTTVPKMLVNIQTQNNVITYAGCITQIYFFLLFVELDNFLLTIMAYDR 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                             CEPNQVIQLTCSDAFLNDLVIYFTLVLLATVPLAG--IFYSYFKIVSSICAISSVHGKYK 236
                                                                     AFSTCASHLSVVSLFYCTGLG----VYLSSAANNSSQASATASVMYTVVTPMVNPFIYSLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650-845-4166
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Hillman, Jennifer L.
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                                ---RILRLFHVATH 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 141
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PATENTIN REL
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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PITLE OF INVENTION: Polynucleotides Encoding Human G-Protein

FITLE OF INVENTION: Coupled Receptor GPR2

NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT:
                                                                                                                                                      124
                                                                                                              184 HQDVMKLACDDIRVN--VVYGLIVIISAIGLDSLLISFSYLL--ILKTVLGLTREAQAKA 239
                                                                                                                                                                                            124 DRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCL 183
                                    240 FGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-LUS
COPTWARE: PATENTIN RELEASE $1.0, VERSION $1.30
                                                                                                                                                                                                                                64 FFLSHLAVVNIAYACNTVPQMLVNLLHPAKPISFAGCMTLDFLFLSFAHTECLLLVLMSY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/01 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                    64 IFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAF 123
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                          ILSVLRLACADTWLNQVVIFEACMFILVGPLCLVLVSYSHILGGILRIQSG----EGRRKA
                                                                                                                                                    DRYVAICHPLRYFIIMTWKVCITLGITSWTCGSLLAMVHVSLILRLPFCGPREINHFFCE 183
                                                                                                                                                                                                                                                                                                                                NESSATYFILIGL---PGLEEAQFWLAFPLCSL-YLIAVLGNLTIIYIVRTEHSLHEPMY 63
                                                                                                                                                                                                                                                                                                            NQTMVTEFLLLGFLLGPRIQ----MLLFGLFSLFYVFTLLGNGTILGLISLDSRLHTPMY 63
FSTCSSHLCVVGLFFGSAIVMYMAPK-SRHPEEQQKVLFLILQFLSTPMLKP
                                                                                                                                                                                                                                                                                                                                                                                        94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAO, LIAN
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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SYSTEM: PC-DOS/MS-DOS
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Best Local
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NFORMATION FOR SEQ
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LENGTH: 296 amino ---
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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184 ILSVLRLACADTWLNQVVIFEACMFILVGPLCLVLVSYSHILGGILRIQSG----BGRRKA 240
                                                                                       184
                                                                                                                                                        124 DRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             64 IFICMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                             64 FFLSHLAVVNIAYACNTVPQMLVNLLHPAKPISFAGCMTLDFLFLSFAHTECLLLVLMSY 123
                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                              8 NQTMVTEFLLLGFLLGPRIQ----MLLFGLFSLFYVFTLLGNGTILGLISLDSRLHTPMY 63
                                                                                                                                                                                                                                                                                                    8 NESSATYFILIGL---PGLEEAQFWLAFPLCSL-YLIAVLGNLTIIYIVRTEHSLHEPMY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LE OF INVENTION: Polynucleotides Encoding Human G-Protein LE OF INVENTION: Coupled Receptor GPR1
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                                                                                     HQDVMKLACDDIRVN--VVYGLIVIISAIGLDSLLISFSYLL--ILKTVLGLTREAQAKA 239
                                                                                                                      DRYVAICHPLRYFIIMTWKVCITLGITSWTCGSLLAMVHVSLILRLPFCGPREINHFFCE 183
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1100 NEW YORK AVE.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATENTIN RELEASE #1.0, VERSION #1.30
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                                                                                                                                                                                                                                                                                                                                                       22.6%; Score 367; DB 32.2%; Pred. No. 3e-26;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                               Matches
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                   120
                                                                                                                                                                                   135 HATVLTLPRVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino STRANDEDNESS:
TOPOLOGY: 11
                                    246 HVCAVFIFYVPFIGL 260
                                                                         178 FSDTRVNEWVIFIMGGLILVI-----PFLLILGSYARIVSSILKVPSSKGICKAFSTCGS 232
                                                                                                             192 CDDIRVN-----VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 245
                                                                                                                                                                                                                                           75 LISTSSMPKMLAIFWENSTTIQEDACLLQMFAIHSLSGMESTVLLAMAFDRYVAICHPLR 134
                                                                                                                                                                                                                          61 CFSSVTIPKLLQNMQNQDPSIPYADCLTQMYFFLLFGDLESFLLVAMAYDRYVAICFPL- 119
                                                                                                                                                                                                                                                                                                                         15 FILIGLEGGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEEMYIFLCMLSGIDI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  1 FLLLGLPIQPEQQNLCYALFLAMYLTTLLGNLLIIVLIRLDSHLHTPMYLFLSNLSFSDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
DPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                HYTAIMSPMLCLALVALSWVLTTFHAMLHTL--LMARLCFCADNVIPHFFCDMSALLKLA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTER READABLE FORM:
HLSVVSLFYGTVIGL 247
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Ruben, Steven M.
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RESULT 13

RESULT 14 US-09-339-115-3

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
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APPLICATION NUMBER: US 0
FILING DATE: 06-JUN-1995
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233
                                                                  178 FSDTRVNEWVIFIMGGLILVI--
                                                                                                                                                                      135 HATVLTLPRVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLA 191
                                                                                                                                                                                                                                                                                                             15 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 74
                                                                                                                                                                                                        61 CESSVTIPKLLQNMQNQDPSIPYADCLTQMYFFLLFGDLESFLLVAMAYDRYVALCEPL-
                                                                                                                                                                                                                               75 LISTSSMPKMLAIFWENSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDRIVAICHPLR 134
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New Jersey
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                            HVCAVFIFYVPFIGL 260
                                                                                                 CDDIRVN-----VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 245
                                                                                                                                       HYTAIMSPMLCLALVALSWVLTTFHAMLHTL--LMARLCFCADNVIPHFFCDMSALLKLA
 HLSVVSLFYGTVIGL 247
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Li, Yi
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36.9%;
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Pred. No. 7.7e-26;
""" amatches 99;
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RESULT 15
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LENGTH: 247 amino acids
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MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
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                                                                                                                                 178 FSDTRVNEWVIFIMGGLILVI---
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                                                                                                                                                                                                                                                                                                                                                61 CESSVTIPKLLQNMQNQDPSIPYADCLTQMYEFLLFGDLESFLLVAMAYDRYVAICFPL- 119
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                              75 LISTSSMPKMLAIFWENSTTIQEDACLLQMFAIHSLSGMESTVLLAMAEDRYVAICHPLR 134
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REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                                                                               1 FLLLGLPIQPEQQNLCYALFLAMYLTTLLGNLLIIVLIRLDSHLHTPMYLFLSNLSFSDL 60
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                                                                                               HVCAVFIFYVPFIGL 260
                                                                                                                                                                                                 HYTAIMSPMLCLALVALSWYLTTFHAMLHTL--LMARICFCADNVIPHFFCDMSALLKLA 177
                                                                                                                                                                                                                               HATVLTLPRVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLA 191
                                                                  HLSVVSLFYGTVIGL 247
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New Jersey
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Ruben, Steven M.
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Li, Yi
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STUART & OLSTEIN
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Search completed: March 26, 2003, 09:58:02
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
SEQUENCE CHARACTERISTICS
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APPLICANT: Soppet
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REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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233
                                   246 HVCAVFIFYVPFIGL 260
                                                                       178 FSDTRVNEWVIFIMGGLILVI-----PFLLILGSYARIVSSILKVPSSKGICKAFSTCGS
                                                                                               192 CDDIRVN-----VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 245
                                                                                                                                            120 HYTAIMSPMLCLALVALSWYLTTFHAMLHTL--LMARLCFCADNVIPHFFCDMSALLKLA
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                                                                                                                                                                                                                 61 CÉSSVTIPKLIQNMQNQDPSIPYADCLTQMYFFLLFGDLESFLLVAMAYDRYVAICFPL- 119
                                                                                                                                                                                                                                          75 LĮSTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDRYVAICHPLR 134
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OPERATING SYSTEM: PC-DOS/MS-DOS
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HLSVVSLFYGTVIGL 247
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Pred. No. 7.7e-26;
5; Mismatches 99;
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39n2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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	Sequence 113, App	Sequence 267, App	Sequence 9, Appli	Seguence 341, App	Sequence 111, App	Sequence 219, App	Sequence 101, App	Sequence 337, App	Sequence 333, App	Sequence 487, App	Sequence 14, Appl	Sequence 263, App	25	Sequence 117, App	89	0	Sequence 115, App	85	Ξ,	10	Sequence 93, Appl	Sequence 261, App	Sequence 265, App	Sequence 335, App	Sequence 81, Appl	Sequence 2, Appli

### ALIGNMENTS

RESULT 1 US-10-012-896-920 TYPE: PRT
ORGANISM: Homo sapiens
JS-10-012-896-920 NUMBER OF SEQ ID NOS: 1011 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 920 LENGTH: 318 FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10 APPLICANT: Meagher, Madeleine Joy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER APPLICANT: APPLICANT APPLICANT: APPLICANT PPLICANT Fanger, Gary R. Wantanabe, Yoshihiro Hural, John McNeill, Patricia D. Houghton, Raymond L. Vinals de Bassols, Carlota Foy, Teresa Skeiky, Yasir A.W. Hepler, William T. Henderson, Robert A. Retter, Marc W. Stolk, John A. Carter, Darrick Application US/10012896 Kalos, Michael D. Harlocker, Mitcham, Jennifer edvick, Thomas Jiangchun US20020183251A1 Craig H. Aijun Yuqiu Susan L.

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US-09-895-793-920; Sequence 920, App.; Publication No.
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Matches 318;
                 Query Match
Best Local Similarity
                                                                                                         SOFTWARE: FastSEQ
SEQ ID NO 920
LENGTH: 318
                                                                                                                                                     FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
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Hepler, William T.
Henderson, Robert A.
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Mitcham, Jennifer L.
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Li, Samuel X.
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o. US20020192763A1
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Pred. No. 2.5e-147;
   Score 1623; DB 9;
Pred. No. 2.5e-147;
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SOFTMARE: FASTSEQ for Windows Version
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
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                                                              Matches
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Best Local Similarity
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CURRENT FILING DATE: 2001-06-29
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
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   MMYDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHE 60
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Kalos, Michael D.
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Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert
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o. US20020193296A1
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PRIOR FILLING DATE: 2000-09-27
PRIOR PELICATION NUMBER: 60/261,776
PRIOR APPLICATION NUMBER: 60/261,776
PRIOR FILLING DATE: 2001-01-16
PRIOR FILLING DATE: 2001-07-13
PRIOR PELICATION NUMBER: 60/313,202
PRIOR FILLING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 60
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Best Local 9
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SEQ ID NO 2
LENGTH: 318
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APPLICANT: CACACE, A.
APPLICANT: BARBER, L.
APPLICANT: KORNACKER, M.G.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY4,
TITLE OF INVENTION: EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNG
FILE REFERENCE: D0039NP
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APPLICANT: MINTI
APPLICANT: RAMAN
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RAMANATHAN, C.S.
HAWKEN, D.R.
CACACE, A.
BARBER, L.
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Pred. No. 2.5e-147;
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SOFTWARE: FAS:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ. ID NOS: 934
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Vedvick, Thomas :
Carter, Darrick
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Hepler, William
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Dillon, Davin
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US-09-780-669-920

Sequence 920, Application Patent No. US20020051977A1

Application US/09780669

GENERAL INFORMATION:

Dillon, Davin C.

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US-09-822-827-920
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US-09-780-669-920
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SEQ ID NO 920
LENGTH: 318
TYPE: PRT
             Sequence 920, Application US/09822827 Patent No. US20020081680A1
GENERAL INFORMATION:
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APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
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Hepler, William
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Carter, Darrick
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; SOFTWARE; PatentIn Ver. ; SEQ ID NO 91; LENGTH: 318; TYPE: PRT; ORGANISM: Homo saplens US-09-886-055-91
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US-09-822-827-920
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
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APPLICANT: STRYER, LUBERT
APPLICANT: ZOZULYA, SERG
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Patent No. US20020132273A1
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Best Local :
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Best Local Similarity
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TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
FILE REFERENCE: 078003-0277150
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CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/886,055
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,812
PRIOR FILING DATE: 2000-06-22
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                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 522
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                                                                    318;
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                                                                  Conservative
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                                                               100.0%; Score 1623; DB 10; 100.0%; Pred. No. 2.5e-147; tive 0; Mismatches 0;
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Pred. No. 2.5e-147;
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LENGTH: 320
TYPE: PRT
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Best Local Similarity
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Vei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Soppet et al.
TITLE OF INVENTION: Human Prostate Specific G-Protein Receptor HPRAJ70
FILE REFERENCE: PF180P1
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PRIOR FILING DATE: 1998-04-01
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FILING DATE: 1999-06-24
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                              MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLIIKTVLGL-TREAQAKAFGTCVSH 246
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Pred. No. 3
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CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 527
LENGTH: 320
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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                             RLFHVA 312
                                                                IGVVLAFYVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVL
                                                                                            VCAVFIFYVPFIGLSMVHRESKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRIL
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
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Carter, Darrick
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Mitcham, Jennifer L.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 983; DB 9;
Pred. No. 3.2e-86;
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US-09-895-793-527

Sequence 527, Applic Publication No. US20 GENERAL INFORMATION:

Application US/09895793

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RESULT 12
US-09-895-814-527
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US-09-895-793-527
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NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 527

LENGTH: 320
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Matches 183;
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/895,793
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ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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                                                                                           RLFHVA 312
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                                                              AMFKIS 309
                                                                                                                          Dillon, Davin C.
Mitcham, Jennifer L.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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Pred. No. 3.2e-86;
4; Mismatches 67;
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Sequence 527,

Application US/09895814

RESULT 13 US-09-759-143-527

Sequence 527, Application US/09759143
Patent No. US20020022248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.

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; ORGANISM: Homo sapiens
US-09-895-814-527
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 527
LENGTH: 320
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/895,814
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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304 AMFKIS 309
                                                                                          247 VCAVFIFYVPFIGLSMYHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRIL 306
                                                                                                                             128 AICHPLRHATVLTLPRVTKIGVÄÄVVRGÄÄLMÄPLPVFIKQLPFCRSNILSHSYCLHQDV 187
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                              RLFHVA 312
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Kalos, Michael D.
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Mitcham, Jennifer L.
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Hepler, William T.
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US-09-730-018-7; Sequence 7, Application US/09730018; Patent No. US20020048777A1
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LENGTH: 320
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                                                                          APPLICANT: Sun, Yongming
TITLE OF INVENTION: Method of Diagnosing, Monitoring,
TITLE OF INVENTION: Treating Prostate Cancer
CURRENT APPLICATION NUMBER: US/09/730,018
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/169,083
PRIOR FILING DATE: 1999-12-06
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CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
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                                                                FILE REFERENCE: DEX-0119
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SOFTWARE: FastSEQ fo:
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LICANT: Hepler, William
LE OF INVENTION: COMPOSITION
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Local Similarity 59.8%;
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                                                                                                                            Cafferkey, Robe
Recipon, Herve
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Retter, Marc W.
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Kalos, Michael D.
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                                                                                                                                            Robert
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Pred. No. 3.2e-86;
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; ORGANISM: Homo sapiens
US-09-730-018-7
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US-09-780-669-527
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             SOFTWARE: Fa
SEQ ID NO 527
LENGTH: 320
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                         APPLICANT: Houghton, Raymond I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
                                                                                CURRENT FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                   NUMBER OF SEQ ID NOS:
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLACDDIRVNYYYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527
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                                                                                                                                                                                                                                                                                       Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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                                                       FastSEQ for
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                                                                                                                                                                McNeill, Patricia
                                                                                                                                                                                 Hural, John
                                                                                                                                                                                            Hepler, William
                                                                                                                                                                                                                                                                                                                                                                  Jiang, Yuqui
                                                                                                                                                                                                                                                       Carter, Darrick
                                                                                                                                                                                                                                                                 Day, Craig H.
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                    Henderson, Robert A.
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                                                                                                                                                                                                                                        i, Samuel
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                                                       Windows Version 3.0
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                                                                                             US/09/780,669
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Pred. No. 3.
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1.2e-86;
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Search completed: March 26, 2003, 10:05:08
Job time : 16 secs
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                                      304 AMFKIS 309
                                                                                                                   307 RLFHVA 312
                                                                             244 IGVVLAFYVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVL 303
                                                                                                                                                                                                Length 320;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein protein search, using sw model

Run on: March 26, 2003, 09:53:07; Search time 46 Seconds (without alignments) 664.581 Million cell updates/sec

Title: Perfect score: US-09-966-459A-2 1623

Scoring table:

Sequence: 1 MAVDPNGNESSATYFILIGL... ..KEIRQRILRLFHVATHASEP 318

Searched: 283224 segs, 96134422 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283224

Minimum DB Maximum DB seq length: 0 length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database PIR\_73:\* pir3:\* pir4:\* pir1:\*

5 No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25			22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	σ	v	4	ω	2	1	NO.	Result
394.5	397.5	399.5	399.5	399.5	401.5	404.5	405	406.5	411	411	411.5	413	415	418.5	420.5	422.5	424.5	425.5	431.5	431.5	432	433.5	434.5	434.5	440	453	477.5	551	acor e	
24.3	24.5	24.6	24.6	24.6	24.7	24.9	25.0	25.0	25.3	25.3	25.4	25.4	25.6	25.8	25.9	26.0	26.2	26.2	26.6	26.6	26.6	26.7	26.8	26.8	27.1	27.9	29.4	33.9	Maten.	
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olfactory receptor	odorant receptor 3	odorant receptor 3	odorant receptor 3	olfactory receptor	olfactory receptor	olfactory receptor	odorant receptor 4	olfactory receptor	olfactory receptor	probable olfactory	chemoreceptor TB33	probable olfactory	odorant receptor 1		olfactory receptor	olfactory factor 0			olfactory receptor	olfactory receptor						olfactory receptor	odorant receptor 8	al pro	pescription	•

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	
285.5	289.5	307.5	310.5	310.5	366	370	371.5	379	379.5	380	386.5	386.5	387.5	388.5	393.5	
17.6	17.8	18.9	19.1	19.1	22.6	22.8	22.9	23.4	23.4	23.4	23.8	23.8	23.9	23.9	24.2	
222	234	264	234	222	318	315	315	317	327	333	312	304	328	315	316	
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D40745	S28999	PC4369	S29000	B40745	JC5202	JC5201	JC4658	D23701	F23701	A23701	A46750	S29709	C45774	JC5836	A57069	
odorant receptor (	G protein-coupled	olfactory receptor	G protein-coupled	odorant receptor (	chemoreceptor TB64	chemoreceptor TB56	olfactory receptor	odorant receptor 3	olfactory receptor	olfactory receptor						

#### ALIGNMENTS

# RESULT 1 A60547

hypothetical protein (HPFH breakpoint 3' region) human (fragment)

C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993
C;Accession: A60547; A60482 R; Feingold, E.A.; Forget, B.G. #text\_change 26-Aug-1999

of fetal

A;Accession: A60547; MOID:90028751; PMID:2478223

A; Molecule type: DNA A; Residues: 1-292 <FEI>

C; Superfamily: olfactory receptor OR14

Query Match Best Local Similarity Matches 114; Conservative 33.9%; pred. No. 41.0%; pred. No. 41.0%; Mismatches Score 551; DB 2; Pred. No. 1.8e-41; Length 292; Indels 22; Gaps 6,

밁 Š 29 LYGIPGLESVQCWIGIPFCAIYLIAMIGNSLLLSIIKSERSLHEPLYIFLGMLGATDIAL 17 LIGHPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILI 76 88

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Ş 밁 266 FYLLAFFSFFTHRFGSH---253 FYVPFIGLSMYHRFSKRRDSPLPVILANIYLLVPPVLN 290 --IPPYIH 288

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odorant receptor 8 - channel catfish
C;Species: Ictalurus punctatus (channel catfish)
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999
C;Accession: E45774

ng, M.M.; Buck, L.; Axel, R.; Chess, A. 1993

R:Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A. Cell 72, 657-666, 1993
A;Title: The family of genes encoding odorant receptors in A;Reference number: A45774; MUID:93201590; PMID:7916654
A;Accession: E45774 the channel catfish.

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A; Residues: 1-307 < RAM>
C; Superfamily: olfactory receptor OR14
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A;Title: Cloning and expression of odorant A;Reference number: S29707; MUID:93149273;
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A; Molecule type: mRNA
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C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Sin
Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Accession: S29710
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                                                                                                                                                                  FFLASLSLLDALFSTAISPKLIADLLYDQKTISFRACMSQLFIEHLFGGVDIVILVAMAY
                                                                                                                                                                               IFICMISGIDILISTSSMPKMLAIFWENSTTIQFDACLIQMFAIHSISGMESTVLLAMAF 123
                                                                                                                                                                                                                                                              GNESSATYFILIGL---PGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IREQFLKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCILIGLMAVVDLSMPIFCVPNMLLSFLPNMKGISLVGCLVQMFCIHCAGTFQSTILLWM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEP 61
                                MSPLLVLACTD--
                                                                HQDVMKLACDDIRVNVVYGLIVI----ISAIGLDSLLISFSYLLILKTVLGLTREAQAKA
                                                                                                 DRYVAICKPLHYLAIMNRRVCITLLIFAWTGGFTHSLIQIVFVYNLPFCGPNVIDHFICD
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FGTCVSHVCAVFIFYVP--FIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCITHIIVMTVSLTFALIAFLSYRI--RNFSPSSRVFLSTMYLFIPSCFNPIIYGVRTKE
                                                                                                                                                                                                                                                                                                              Similarity
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Y 34.48;
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                                -TYFIGLTVIANGGYNCIVIFTLLLG-SYGIILRSLKTQSQEGRRKA
                                                                                                                                                                                                                                                                                                       27.9%;
33.6%;
                                                                                                                                                                                                                                                                                                64;
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                                                                                                                                                                                                                                                                                                            Score 453; DB 2;
Pred. No. 9.8e-33;
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Pred. No. 6.7e-35;
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PMID:7678922
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R;Nef, P.; Hermans-Borgmeyer, I.; Artieres-Pin, H.; Beasley, L.; Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992
A;Title: Spatial pattern of receptor expression in the olfactory A; Reference number: A46247; MUID:93028384; PMID:1384038
A; Accession: A46247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
A46247
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                                                                                                                     R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors:
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: I23701
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                               olfactory receptor 114 - rat
c;Species: Rattus norvegicus (Norway ra
C;Date: 22-7an-1993 #sequence_revision
C;Accession: 123701
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C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
C;Keywords: G protein-coupled receptor
                               A;Cross-references: GB:M64391; NID:g205843; C;Superfamily: olfactory receptor OR14
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A;Note: sequence extracted from NCBI backbone (NCBIP:115362)
C;Superfamily: olfactory receptor OR14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-312 <NEF>
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                                                                             A; Molecule type: mRNA
A; Residues: 1-312 <BUC>
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Best Local S
Matches 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHEPMYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTV 117
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on 22-Jan-1993 #text_change
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                                                           PIDN:AAA41754.1; PID:g205844
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1992
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receptor;

transmembrane

protein

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237

182

179

123

120

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F;26-48/Domain: transmembrane #status predicted <TM1> F;58-79/Domain: transmembrane #status predicted <TM2> F;101-120/Domain: transmembrane #status predicted <TM3> F;101-164/Domain: transmembrane #status predicted <TM4> F;197-218/Domain: transmembrane #status predicted <TM5> F;237-260/Domain: transmembrane #status predicted <TM6> F;277-292/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change
C;Accession: JC5624; $58003
R;Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M.
Biochem. Biophys. Res. Commun. 237, 283-287, 1997
A;Title: Molecular cloning and chromosomal mapping of olfactory
A;Reference number: JC5624; MOID:97415789; PMID:9268701
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submitted to the EMBL Data Library,
A;Description: Male germ cells from
A;Reference number: S57995
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                                                                                                                                                                                                                                                                                                                                                        A; Description: involved in control of sperm physiology
                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 19p13.1 C; Function:
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A;Residues: 126-282 <VAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S58003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-319 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Cross-references: GB:Y10530; NID:92792017; PIDN:CAA71558.1; PID:92792018; Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M. ubmitted to the EMBL Data Library, July 1995; Description: Male germ cells from several mammalian species express a spipescription:
                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                 Superfamily: olfactory receptor OR14 Reywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:X89677; NID:g902337; PIDN:CAA61824.1;
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Best Local Similarity
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                                                                                     Matches
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                     7 GNESSATYFILIGL---PGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMY 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDRYV 127
GNDTQISEFLLLGFSQEPGLQPFLFGL---FLSMYLVTVLGNLLIILATISDSHLHTPMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRNRDMKRALIRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAKAFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVIG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AICFPLRYTTIMS ----TKFCASLVLLLWMLTMTHALLHTL --LIARLSFCEKNVILHFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AICHPLRHATVLTLPRVTKIGVAAVV------RGAALMAPLPVFIKQLPFCRSNILSHSY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLSFSDLCFSSVTMPKLLQNMQSQVPSISYTGCLTQLYFFMVFGDMESFLLVVMAYDRYV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDISALLKLSCSDIYVNELMIYILGGLIIII-----PFLLIVMSYVRIFFSILKFPSIQD
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                                                                                                       Similarity
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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33.5%;
                                                                                                     26.8%;
                                                                                                                                                                                                                                                                                                                 receptor; transmembrane
                                                                                 . 70;
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                                                                               Score 434.5; DB 2;
Pred. No. 4.5e-31;
0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 434.5; DB 2;
Pred. No. 4.4e-31;
                                                                                                                                                                                                                                                                                                                 protein
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                                                                               Gaps
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                                                                                                     RESULT 8
G45774
               odorant receptor 202 - channel catfish C;Species: Ictalurus punctatus (channel C;Date: 20-Feb-1995 #sequence_revision: C;Accession: G45774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-312 < RAM>
C; Superfamily: olfactory receptor OR14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Raming, K.; Krieger, J.; Strotmann, J.; E Nature 361, 353-356, 1993
A;Title: Cloning and expression of odorant A; Reference number: S29707; MUID:93149273; A; Accession: S29708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              123 YVAICLPLHYTSIMSPKFCVCLGSLSWVFNVLISMLHTLLLARLSFCKDNVIPHFFCDIS 182
                                                                                                                                                                                                                                300
                                                                                                                                                                                        296
                                                                                                                                                                                                                                                                         238
                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                              186 DVMKLACDDIRVN-----VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 YVAICHPLRHATYLTLPRYTKIGVAAVYRGAALMAPLPYFIKQLPFCRSNILSHSYCLHQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238
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                                                                                                                                                                                                                                                                                                                                                           183 ALLKLACSDTYINELMIFILGGLLIVI-----PFLLIVMTYVQIVCSILKVPSTRAIYKI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296
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                                                                                                                                                                                      DIKEALVRV 304
                                                                                                                                                                                                                             EIRQRILRL 308
                                                                                                                                                                                                                                                                         FSTCGSHLSTVSLFYGTVIGLYLCP--SANNSTVKETVMAMMITVVTPMLNPFIYSLRNR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSNLSFSDLCFSSVTMPKLLQNMQNQDTSITYTGCLTQMYFSMVFAGMEIFLLVSMAYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTVISOFILLGLP--IPPEHWHLFYTLLLAMYLTTILGNLIIILLLLDSNLHIPMYLF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFICMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAF
                                                                                                                                                                                                                                                                                                                 FGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NESSATYFILIGLPGLEEAQFWLAF--PLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor OR12 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELNQVIQLACSDSFLNHMVIYFTVALLGGGPLTGIL--YSYSKIISSIHAISSAQGKYKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
  Dowling,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.7%; Score 433.5; DB 2; 32.0%; Pred. No. 5.4e-31;
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Buck,
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Axel,
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receptors. PMID:7678922

Indels Length

17;

Gaps

5

312;

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Kub1ck,

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Baumstark,

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20-Feb-1995 #text\_change

04-Sep-1998

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Chess,

catfish)

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A; Experimental source: olfactory epithelium A; Note: sequence extracted from NCBI backbone C; Superfamily: olfactory receptor OR14 C; Keywords: olfaction; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A45774; MUID:93201590; PMID:7916654 A;Accession: G45774
                                                                                                                                                                                                                                                                                                                                                                                        R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors:
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: E23701
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C; Keywords: G
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                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-310 <BUC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Date: 22-Jan-1993 #sequence_revision
C; Accession: E23701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 72, 657-666, 19 A; Title: The family
                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              olfactory receptor I3 - rat
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Best Local S
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 YVAICHPLRHATVLTLPRVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYC
                                                                                                                                                     NESSATYFILIGLPGLEEAQ--FWLAFPLCSLYLIAVLGNUTIIYIVRTEHSLHEPMYIF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSTCSSQLIITLFFLPRCLNYLSSSLGIH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HQDVMKLACDDIRVNVVYGLIVIISAIGL---DSLLISFSYLLILKTVLGL-TREAQAKA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEGNITNVKNEVILGEPGLPPNYYGLVSVVMFFVYVCTLIGNCTFFTLFLREKSLQKPMY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNGNESSATTFILIGLEGLEEAQFWL-AFPLCSLYLIAVLGNLTIIYIVRTEHSLHEEMY 63
                                                       LSNLSFSDLCFSSVTMPKLLQNMRSQDTSIPYGGCLAQTYFFMVFGDMESFLLVAMAYDR
                                                                                          LCMLSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDR 125
                                                                                                                                NOTE IT OF LLIGLE I PEEHOHLEY ALELY -- MYLTTILGULLII VLVQLDSQLHTPMYLF
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93; Conservative
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                protein-coupled receptor; transmembrane
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
                                                                                                                                                                                                                       26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.6%; Score 432; DB 2; 29.7%; Pred. No. 7.8e-31; tive 75; Mismatches 127
                                                                                                                                                                                                         71;
                                                                                                                                                                                                       Score 431.5; DB 2
Pred. No. 8.1e-31;
1; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rat)
on 22-Jan-1993 #text_change
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                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 328
                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                       13;
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R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
Cell 67, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors:
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: A37286
                                                                                                                                                                   RESULT 11
A37286
                                                                                      olfactory receptor II5 - rat
C;Speckes: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22
C;Accession: A37286
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olfactory receptor - human c;Speckes: Homo sapiens (man) C;Speckes: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999 C;Accession: S20572
R;Parmentier, M.; Libert, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eg;
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A; Residues: 1-314 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Expression of members of the putative olfactory A; Reference number: $20571; MUID:92131132; PMID:1370859 A; Accession: $20572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:X64994; NID:g32085; PIDN:CAA46127.1; PID:g32086; Superfamily: olfactory receptor OR14; Reywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
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294 NRDMKGALSRVIH
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:: ::|:
KRALIRV 302
                                       TKEIRQRILRLFH 310
                                                                                                                                              SALLKLAFSDTRVNEWVIFIMGGLILVI----PFLLILGSYARIVSSILKVPSSKGICK
                                                                                                                                                                                                                                                                                     NLSFSDLCFSSVTIPKLLQNMQNQDPSIPYADCLTQMYFFLLFGDLESFLLVAMAYDRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGSHLSYVSLFYGTIIGLYLCP--AGNNSTVKEMVMAMMYTVVTPMLNPFIYSLRNRDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFG
                                                                           AFSTCGSHLSVVSLFYGTVIGLYLC---SSANSSTLKDTVMAMMYTVVTPMLNPFIYSLR
                                                                                                        AFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPL-PVILANIYLLVPPVLNPIVYGVK 297
                                                                                                                                                                              QDVMKLACDDIRVN-----VVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAK 238
                                                                                                                                                                                                                  AICFPL-HYTAIMSPMLCLALVALSWVLTTFHAMLHTL--LMARLCFCADNVIPHFFCDM
                                                                                                                                                                                                                                                    ATCHPLRHATVLTLPRVTKIGVA---AVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLH
                                                                                                                                                                                                                                                                                                                     MLSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDRYV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                            109;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Pred. No. 8.2e-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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22-Jan-1993 #text\_change

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molecular

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R:Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A. Cell 72, 657-666, 193
A;Title: The family of genes encoding odorant receptors in the A;Reference number: A45774; MUID:93201590; PMID:7916654
A;Accession: H45774
A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-321 <NGA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M64392; NID:g205845; PIDN:AAA41755.1; PID:g205846 C;Superfamily: olfactory receptor OR14 C;Keywords: G protein-coupled receptor; transmembrane protein
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                                              C; Reywords: olfaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               odorant receptor 3 - channel catfish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-314 <BUC>
                                                                                                                                                                                                                                                                                                                                                                             Experimental source: olfactory epithelium; Rote: sequence extracted from NCBI backbone; Superfamily: olfactory receptor OR14
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
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                                                         133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 IHKIFSTCGSHLSVVSLFYGTIIGLYLCP--SANNSTVKETVMAMMYTVVTPMLNPFIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 YVAICHPLRHATVLTLPRVTKIGVAAVVRGAALM---APL-PVFIKQLPFCRSNILSHSY 181
                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                          14 TNATFIRPSTFYITGLYNIPHAKYYYLF-LCFVYTVTFLGNSFIMGTIYLARSLHTAKYI
                                                                                                                                                                                                                                              10 SSATY-----FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 NESSATYFILIGLPGLEEAQ--FWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIF
QDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLI----LKTVLGLTREAQAKAF
: ||||:| : | : : : : || ||: | | : | ||
                                                                                                                                                                     FLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFD
                                                                                            RYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLH
                                                                                                                                 AVFNLALSDLCGSSALIPKLLDMLLFENQSISYEACLSNMFFVYCFMTLQCLTLLALAYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDISPLIKLSCSDTHVNELVIFVMGGLVIVIPFV-----LIIVSYARVVASILKVPSVRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NQTVISQFLLLFLPIPSEHQHVFYALF--LSMYLTTVLGNLIIILLHLDSHLHTPMYLF
                                                       RLIAICYPLRYHAIVTKAAMIFIIGAMWVLSVSVNAVLVALITRLSFCRSTTVYSYFCDH
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                                                                                                                                                                                                                                                                                     102;
                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                            transmembrane protein
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                                                                                                                                                                                                                                                                                                     Score 424.5; DB 2;
Pred. No. 3.5e-30;
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                                                                                                                                                                                                                                                                                     Mismatches
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                   240
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R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors:
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: B37286
                                                                                                                                                                                                                                                                                              olfactory receptor OR5 - rat
C;Species: Rattur ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Nature 361, 353-356, 1993
A;Title: Cloning and expression of odorant receptors.
A;Reference number: S29707; MUID:93149273; PNID:7678922
A;Accession: S29711
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                                                                                                                                                                 Nature 361, 353-356, 1993
A; Title: Cloning and expression of odorant
A; Reference number: S29707; MUID:93149273;
                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 10
C;Accession: S29707; B37286
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A; Residues: 1-305 < RAM>
C; Superfamily: olfactory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 10
C;Accession: S29711
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                                                                                                      A; Molecule type: mRNA
A; Residues: 1-314 < RAM>
                                                                                                                                              A; Accession: S29707
                                                                                                                                                                                                             R;Raming, K.; Krieger, Nature 361, 353-356, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YTTSSVPSTLVSLISKKRNISFSGCTVQMFVGFAMGSTECLLLGMMAFDRYVAICNPLRY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKEIRORI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLGLSGYPKTEILYFVIVLVMYLVIHTGNGVLIIASIFDSHLHTPMTFFLGNLSFLDIC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPIYKLACNDNTINSINGNVCTATLLYFPLILIIASYVCIGFALQKIAHGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTVVVIFYGTIFSM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCAVFIFYVPFIGLSMVHRFSKRRDSPL-----PVILANIYLLVPPVLNPIVYGVK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKLACADISLNIVTMVISNMAFLVLPLLLIFFSYVLILYTILRMNSASGRRKAFSTCSAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVIMSKEVYVSMASASWFSGGINSVVQTSLAM-----RLPFCGNNVINHFTCEVLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRQRILRLF-HV 311
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                                                                                                                                                                                                                                 J.; Strotmann, J.; Boekhoff, I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor OR14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.0%; Score 422.5; DB 2; 32.8%; Pred. No. 5e-30; tive 61; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -YAKPKSQDLTGKDKFQTSDKIISLFYGVVTPMLNPIIYSLR
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                                                                                                                                                                                                                                   Kubick,
                                                                                                                                                                                                                                   S.; Baumstark,
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A;Cross-references: GB:M64375; NID:g205811; PIDN:AAA41738.1; PID:g205812
C;Superfamily: olfactory receptor OR14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 193-236 < BUC>
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                                                                                                                                                                                                                                                                                                                                                                                CTOSS-references: EMBL:X80671; NID:g517365; PIDN:CAA56697.1; PID:g517366;Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M. ubmitted to the EMBL Data Library, July 1994
                                                                                                                                                                                                                                ; Molecule type: mRNA
Residues: 1-309 <GA2>
Cross references: EMBL: X80671; NID: 9517365; PIDN: CAA56697.1; PID: 9517366;
Superfamily: olfactory receptor OR14
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Matches 104;
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Residues: 1-309 <GAT>
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Accession: S51356
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65 SSLSEVDLCYSTVITPKMLVNFLGKKNFITYSECMAQFFFFAIFVVTEGYLLTVMAYDRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NESSATYFILIGLEGLEEAQ--FWLAFFLCSLYLIAVLGNLTIIYIVRTEHSLHEFMYIF 65
                                  CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDRY 126
                                                                                               GNESSATYFILIGLPGLEEAQFWLAFFLCSLYLIAVLGNLTIIIYVRTEHSLHEPMYIFL 66
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                                                                        GNHSAVVVFVLVGLTKQPELLLPLFFLFLVIYVLTVVGNLGMILLIIVSPLLHTPMYYFL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQTVISQFLLLGLPIPPEHQHVFYALF--LSMYLTTILGNLIIILLLLLDSHLHTPMYLF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IR 302
                                                                                                                                                                         Similarity
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                                                                                                                                                   25.8%;
llarity 33.0%;
Conservative 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor proteins. Expression, characterization and partial purificate S51356; MUID:95045546; PHID:7957207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lancet, D.; Natochin, M.
                                                                                                                                                       63;
                                                                                                                                                   Score 418.5; I
Pred. No. 1.1e:
63; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      expression,
                                                                                                                                                                         1.1e-29;
                                                                                                                                                                                          DB 1;
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290 IYSLRNKDVKKALGR 304
                                                            234
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                VYGVKTKEIRQRILR 307
                                                                                                                                      SHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIG--LDSLLISFSYLLILKTVLGL-TRE
                                                                                                                                                                                     VAICRPLLYNVIMS-SRICSLLVLVAFSLGLFSAVVHTSAMM------NLSFCKSYII 175
                                                                                                                                                                                                                    VAICHPLRHATVLTLPRVTKIGV----
                                                            GRSKAFGTCSSHLMAVGIFFGSITFMYLKPSSSNSLEQEK----VSSVFYTTVIPMLNPL 289
                                                                         AQAKAFGTCVSHVCAVFIFY--VPFIGLSMYHRFSKRRDSPLPVILANIYLLVPPVLNPI 292
                                                                                                                        SHYFCDALPLIKLACSNTHLNEL--LIFIIGGLNTLVPTLAVAISYVFIFCSILRIRSSE
                                                                                                                                                                                                                    --- AAVVRGAALMAPLPVFIKQLPFCRSNIL 177
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Search completed: March 26, 2003, 09:57:05
Job time: 48 secs

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OM protein protein search, using sw model

Run on: March 26, 2003, 09:48:21; Search time 25 Seconds (without alignments) 527.579 Million cell updates/sec

US-09-966-459A-2 1623

Title: Perfect score: Sequence: 1 MMVDPNGNESSATYFILIGL.....KEIRQRILRLFHVATHASEP 318

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Result
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09h255 homo 09h344 homo 09h344 homo 09h344 homo 09h341 homo 09h341 homo 09h341 homo 09h341 homo 09h341 homo 09yk12 homo 09yk12 homo 09yspi homo 09yspi homo 09yspi homo 09yspi homo 09yspi homo 09yspi homo 095275 mus 095271 homo 095273 rattt 015622 homo 095371 homo 095374 homo 095371 homo	3
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sapien	

4 4	42	40	39	37	334
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313 313	318	311 313.	318 311	312	311
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OZB6_HUMAN OLF5_RAT	OAH1_HUMAN O5B2_HUMAN	OLF1_CANFA OLFD_CANFA	OLF1_CHICK O8B8_HUMAN	O2J3_HUMAN	O5P3_HUMAN OLF4_CHICK
	Q9y4a9 homo sapien				

### ALIGNMENTS

NOREZ_HUMAN STANDARD; PRT; 320 AA.  OKEZ_HUMAN STANDARD; PRT; 320 AA.  OKEZ_HUMAN STANDARD; PRT; 320 AA.  16-CCT-2001 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) 15-CVT-2001 (Rel. 40, Last annotation update) 15-CVT-2001 (Rel. 40, Last annotation update) 15-CVT-2001 (Rel. 41, Last annotation update) 15-CVT-2001 (Rel. 40, Last annotation update) 16-CVT-2001 (Rel. 40, Last annotation update) 17-CVT-2001 (Rel. 40, Last annotation update) 18-CVT-2001 (Rel. 40, Last annotation update) 19-CVT-2001 (Rel. 40, Last annotation update) 19-CVT-200	AC 091255; DT 16-OCT-2001 (Rel. 40, Cr. DT 16-OCT-2001 (Rel. 40, Cr. DT 16-OCT-2001 (Rel. 40, Cr. DT 15-JUN-2002 (Rel. 41, La. DT 15-JUN-2006; ROBILEZ (REL) (RELEADED (REL) (RE
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RESULT 2
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
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                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                   OR51E2.
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AF369708;
AY033942;
BC020768;
                                                                                                                                                                  IGVVLAFTVPLIGLSVVHRFGNSLHPIVRVVMGDITLLLPPVINPIIYGAKTKQIRTRVL
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                                       40, Created)
40, Last sequence update)
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r 51E2 (G-protein coupled receptor RAIc).
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5 (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (PO
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC...)
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5 (POTENTIAL).
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3 (POTENTIAL).
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        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Identification of a novel G-protein distinct brain regions and a defined Recept. Channels 6:141-151(1998).
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - ! - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raming K., Konzelmann S., Breer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99131082; PubMed=9932290;
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RLFHVA 312
                                       IGVVLAFYVPLIGLSVVHREGNSLDPIVHVLMGDVYLLLPPVINPIIYGAKTKQIRTRVL
                                                                                                         MKLACDDIRVNYYYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH
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                                                    MKLAYTDTLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSH
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59.8%;
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
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CYTOPLASMIC (1
6 (POTENTIAL)
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4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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olfactory zone.";
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2e-67;
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Best Local 9
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SEQUENCE
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Q9H344;
                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane;
Multigene family; Olfaction.
                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                           DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF137396; AAG41678.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor genes flanking clusters.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bulger M., Bender M.A., van
Felsenfeld G., Groudine M.,
"Comparative structural and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc.
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L6-OCT-2001 (Rel.
L6-OCT-2001 (Rel.
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION:
MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFDRYV
                                     NESSATYFILIGLPGLEEAQFWLAPPICSLYLIAVIGNLTIIYIVRTEHSLHEPMYIFLC
                      NVTHPAFFLLTGIPGLESSHSWLSGPLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFLS
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                                                                                  Similarity
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PUTATIVE ODORANT RECEPTOR.
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                                                                   Score 872.5; DB 1;
Pred. No. 3.4e-59;
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Multigene
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                                                                                                                                                                                                                                                                                                                                                       Pfam;
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InterPro; IPR000276; GPCR_R
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                                              use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Pfam; PF00001; 7tm_1;
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                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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            GPCR_Rhodpsn
                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
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                                                                                                                                                                               U.S.A. 97:14560-14565(2000).
                                                                                                                                                                                                                                                                                                                                                (HOR5'betal4).
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                                                                                                                                                                                                              Hardison R.; functional analysis of the olfactory
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                       human and mouse
                                                                                                                                                                                                                                        Doorninck J.H., Wertman
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Pred. No. 1.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae
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                                                           http://www.isb-sib.ch/announce/
                                                                                                                                                                                                   beta-globin
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Best Local S
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Q9H341;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
15-JUN-2002 (Rel. 41, Last annotation updat
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Multigene
                                                                           SEQUENCE FROM N.A. MEDLINE-20570519;
                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                   OXM1_HUMAN
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2; PS00237; (

3; PS50262; (

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G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane;
Olfaction.
                                                                              PubMed=11121057;
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Primates;
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7 (POTENTIAL)
Hardison R.;
functional analysis of the c
                                                             Doorninck
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CYTOPLASMIC (F
6 (POTENTIAL).
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Pred. No. 1.96
'0; Mismatches
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                     PRT;
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                                                           J.H., Wertman
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PRINTS; PR00237; GPCRRHODOPSN
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane;
Multigene family; Olfaction.
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by non-profit institutions as long as its content is in
ified and this statement is not removed. Usage by and for con
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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 annotation update
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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3 (POTENTIAL).
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Pred. No. 4.4
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Multigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lehrach H., Olender Z., Gluesman G., Lancet D., Shamir R
DEFOG: a practical scheme for deciphering families of g
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: PUTATIVE ODORANT RECEPTOR.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                     FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 74
                                                                                                                                       LLSTTTVPKALAIFWLQAHNIAFDACVTQGFFVHMMFVGESAILLAMAFDRFVAICAPLR
                YVPFIGLSMYHRFSKRRDSPLPVILANIYLLVPFVLNPIVYGVKTKEIRQRIL-RLFHVA
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YVPSFFTLLTHHFGRNIPQHVHILLANLYVAVPPMLNPIVYGVKTKQIREGVAHRFFDIK
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                                                                                                                         YTTVLTWPVVGRIALAVITRSFCIIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACAD
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pS00237; G_PROTEIN_RECEP_F1_1;
pS50262; G_PROTEIN_RECEP_F1_2;
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Pred. No. 6.56
57; Mismatches
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M., O'Brien J.K., Radelof U
., Lancet D., Shamir R.;
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OYA1_HUMAN
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                         Multigene
                                                                                                                                                                                                                                                                                                                              G-protein
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MEDLINE-99443868; PubMed-10512676;
Feingold E.A., Penny L.A., Nienhui
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6-OCT-2001
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ngold B.A., Penny L.A., Nienhuis A.W., Forget B.G.; olfactory receptor gene is located in the extended human bin gene cluster and is expressed in erythroid cells.*; omics 61:15-23(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: PUTATIVE ODORANT RECEPTOR.
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0001; 7tm_1; 1.
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   STANDARD;
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Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE
modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                   of odorant receptor genes.";
Proc. Natl. Acad. Sci. U.S.A.
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"Conservation of sequence and structure
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-99238494; PubMed-10220430;

MEDLINE-99238494; PubMed-10220430;

Van Doorninck J.H., Saitoh N., Telling A.,
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                             Bulger M., v
Bender M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Olfactory receptor 51B2 (HOR5'beta3).
                                                                   rhis
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                                            European Bioinformatics Institute.
                                                      SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the ED
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Axel R., Groudine M.;
A. 96:8307-8307(1999).
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Pred. No. 2.6e-50;
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B3A93279352D513C CRC64;
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PRINTS; PR00237; GPCRRHODDPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane;
Multigene family; Olfaction.
                                                 SEQUENCE OF 70-287 FROM N.A. FUChS T., MALECOVA B., Linhart C., SI Shmulevich D., Elkon R., Steinfath M Lehrach H., Olender Z., Gluesman G.,
                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                               OYE6_HUMAN
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(Rel. 41, Last sequence up
(Rel. 41, Last annotation
eceptor 52E6.
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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BY SIMILARITY.
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CYTOPLASMIC
2 (POTENTIAL
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Pred. No. 2.6e-48;
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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ODA1160267778EDD CRC64;
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        M., O'Brien J.K., Radelof U.,
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OXB4\_HUMAN Q9Y5P0; 16-OCT-2001

(Rel. 40, Created)

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RESULT 11
OXB4_HUMAN
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-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycopr
Multigene family; Olfaction.
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NCBI_TaxID=9600;
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of odorant receptor genes.";
Proc. Natl. Acad. Sci. U.S.A. 96:5129-5134(1999)
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Bender M.A.,
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MEDLINE-99238494; PubMed-10220430;
Bulger M., van Doorninck J.H., Saitoh N.
Bender M.A., Felsenfeld G., Axel R., Grc
"Conservation of sequence and structure
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Felsenfeld G., Groudine M.,
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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  Similarity
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.., Felsenfeld G., Axel R., Groudine M.
. Acad. Sci. U.S.A. 96:8307-8307(1999)
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Axel R., Groudine M.;
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InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral r
SIMILARITY: BELONGS TO FAMILY 1
                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                     FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ы
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTPLRYNCILINGRVMNIGLGVLMRGFMSILPIILSLYCYPYCGSRALLHTFCLHQDVIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSAGPFLLTGFLGSEAVHYRISMSFFVIYFSILFGNGTLLVLIWNDHSLHEPMYYFLAML
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                                                                                                        PS00237; G_PROTEIN_RECEP_F1_1; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                     famil
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AR LOCATION: Integral membrane
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Olfaction.
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annotation
                                                                                              Transmembrane;
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CYTOPLASMIC (
4 (POTENTIAL)
                                EXTRACELLULAR
                                                     CYTOPLASMIC
                                                                          EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                      (POTENTIAL)
                                          (POTENTIAL)
                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                     on update)
                                                                                                                                                                                                                                                                                OF G-PROTEIN COUPLED RECEPTORS
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            (POTENTIAL)
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                                                    (POTENTIAL).
                                (POTENTIAL
                                                                        (POTENTIAL)
                                                                                             Glycoprotein;
                                                                                                                                                                                                                                                                                           protein
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Best Local Sin
Matches 114;
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                              between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by
                                                                                                                             "Spatial pattern of receptor expression in the olfactory epithelium. Proc. Natl. Acad. Sci. U.S.A. 89:8948-8952(1992).
-i- FUNCTION: PUTATIVE DORANT RECEPTOR.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-93028384; PubMed-1384038;
Nef P., Hermans-Borgmeyer I., Art
Dionne V.E., Heinemann S.F.;
 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                            OLFR15
                                                                                                                                                                                                                                                                                                     Olfactory
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01-MAR-1992 (Rel. 21, 0
01-NOV-1995 (Rel. 32, 1
15-JUL-1998 (Rel. 36, 1
                                                                                                                                                                                                                                                                                                                                                                 OL15_MOUSE
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                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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Rodentia;
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5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
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Pred. No. 1
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CYTOPLASMIC (
                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                 312
                    (See http://www.isb-sib.ch/announce/
                                     There are no rest
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.3e-28;
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                                                                                                                                                                                           H., Beasley L.,
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RESULT 14
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ID 05F1_HUMAN
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Best Local :
                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
        SEQUENCE OF 68-283 FROM N.A. MEDILINE-99005533; PubMed-9787077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                             Homo sapiens (Human)
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MGD; MGI:106182; Olfr15.
InterPro; IPR000276; GPCR_Rh
                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Difactory receptor 5F1 (Olfactory receptor 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
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                                                                                                                                                                                                                                                                VEGRRKAFNTCVSHLVVVFLFYG-----SAIYGYLLPAKSSNQSQGKFISLFYSVVTPMV
                                                                                                                                                                                                                                                                              REAQAKAFGTCVSHVCAVFIFTVPFIGLSMVHRF---SKRRDSPLPVILANIXLLVPPVL | : | : | : | : | : | : | : | : |
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Glusman
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                                                                                                                                                            STANDARD;
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Primates;
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Ben-Arie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 440;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCHAC. . ) (POTENTIAL).
; 8D3877EBBF51E132 CRC64;
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7 (POTENTIAL)
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                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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InterPro; IPRO00276; GPCR_Rhodpsn.
Pfam; PRO0001; 7tm_1; 1.
PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PR00237; GPCRTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycopi Multigene family; Olfaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUCHS T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R., Shmullevich D., Elkon R., Steinfath M., O'Enrien J.K., Radelof U., Lehrach H., Olender Z., Gluesman G., Lancet D., Shamir R.; "DEFOG: a practical scheme for deciphering families of genes."; submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PUTATIVE DOCARAW RECEPTOR.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Genomics 53:56-68(1998)
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236 QAKAFGTCVSHVCAVFIFYVP--FIGLSMVHRFSKRRDSPLFVILANIYLLVPFVLNPIV
                                            185 FKLSCSDTILKESISSILAGVNIVGTLLVILS:
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                                                                                                                                  AICRPLLYSLIMSRTVYLKMAAGAFAAGLLNFMVNTSHVSSLSFCDSNVIHHFFCDSPPL
                                                                                                                                                                            AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 187
                                                                                                                                                                                                                                                                  MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLIQMFAIHSLSGMESTVLLAMAFDRYV 127
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P23273;
01-NOV-1991
01-NOV-1991
01-JUL-1993
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TRANSMEM
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence up
01-JUL-1993 (Rel. 26, Last annotation
Olfactory receptor-like protein I14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M64391; AAA41754.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         basis for odor recognition. Cell 65:175-187(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buck L., Axel R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91191556; PubMed-1840504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                           RANSMEM
                                                                                                                                                                                                                      MAIN :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: PUTATIVE ODORANT RECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l multigene family may encode odorant receptors: a molecular
or odor recognition.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00237; G_PROTEIN_RECEP_F1_1; 1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
n coupled receptor; Transmembrane;
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IPR000276; GPCR_Rhodpsn.
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                                                                                                35718 MW;
                        26.8%;
33.5%;
                      Score 434.5;
Pred. No. 4.
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
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N-LINKED (GLCNAC. . .)
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                           4.2e-26;
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                                              Length
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Search completed: March 26, 2003, 09:53:02 Job time : 26 secs	292 LRNRDMKRALIRV 304	296 VKTKEIRQRILRL 308	234 IXKVFSTCGSHLSVVTLFYGTIFGIYLCPSGNNSTVKEIAMAMMTTVVTPMLNPFIXS 291	236 QAKAFGTCVSHVCAVFIFYVPFIGLSMVHRESKRRDSPLPVILANIYLLVPPVLNPIVYG 295	179 CDISALLKLSCSDIYVNELMIYILGGLIIIIPFLLIVMSYVRIFFSILKFPSIQD 233	WYGLIVIISAIGL	125 AICPPLRYTTIMSTRECASLVLLLWMLTMTHALLHTLLIARLSFCEKNVILHFF 178	128 AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSY 181	65 NISFSDICESSVTMPKILQNNQSQVPSISYTGCLTQLYFFMVFGDMESFILLVVMAYDRYV 124	68 MLSGIDILISTSSMPKMLAIFWENSTTIQPDACLLQMFAIHSLSGMESTVLLAMAFDRYV 127	5 NQTLILEFLLLGLPIPSEYHLLFYALFLAMYLTIILGNLLIIVLVRLDSHLHMPMYLFLS 64
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1623:
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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L Q8VBV9
L Q8VF09
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# ALIGNMENTS

RESULT 1  (ABYCB6 PRELIMINARY; PRT; 317 AA.  AC OBTCB6; DT 01-JUN-2002 (TIEMBLEE1. 21, Carated) DT 01-JUN-2002 (TIEMBLEE1. 21, Last sequence update) DE Hypothetical 51.3 Na protein. OS Homo saplens (Human). OS Homo saplens (Human). OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Euteleostomi; OX KCBL_TaxID-9606; RN [1] RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RP SEQUENCE STORM N.A. RP SEQUENCE STORM N.A. RP SEQUENCE STORM N.A. RP SEQUENCE 317 AA; 35271 MM; BC7293AA7FBCA95C CRC64; DE SEQUENCE 317 AA; 35271 MM; BC7293AA7FBCA95C CRC64;  Query Match Poloce Protein. SQ SEQUENCE 317 AA; 35271 MM; BC7293AA7FBCA95C CRC64;  Query Match Poloce Protein. SQ SEQUENCE 317 AA; 35271 MM; BC7293AA7FBCA95C CRC64;  Query Match Poloce Protein. SQ SEQUENCE 317 AA; 35271 MM; BC7293AA7FBCA95C CRC64;  Query Match Poloce Protein. SQ SEQUENCE 317 AA; 35271 MM; BC7293AA7FBCA95C CRC64;  Query Match Poloce Protein. SQ SEQUENCE 317 AA; 35271 MM; BC7293AA7FBCA95C CRC64;  Query Match Poloce Protein. SQ SEQUENCE 317 AA; 35271 MM; BC7293AA7FBCA95C CRC64;  Query Match Poloce Protein. SQ SEQUENCE 317 AA; 35271 MM; BC7293AA7FBCA95C CRC64;  Query Match Poloce Protein. SQ SEQUENCE SQ Protein. SQ SEQUENCE 317 AA; 35271 MM; BC7293AA7FBCA95C CRC64;  Query Match Poloce Protein. SQ SEQUENCE SQ Protein. SQ SEQ																									
PRELIMINARY; PRT; 317 AA.  BTCB6 BTCB6 PTCB6 PTCB6 1-JUN-2002 (TTEMBLrel. 21, Last sequence update) 1-JUN-2002 (TTEMBLRel. 21, Last seq	Qy	В	Qy	Db	Qy	В	Qy	Ma	P 10	So	X :	DR E	2 3	2 2	8 P	RN	ò	88	3 8	DE	D.		ج م	ij	RESU
	CLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLFREAQAKAFG	AFDRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSY	AFDRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSY	MYIFICMLSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQMFAIHSLSGMESTVILAM	MYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAM		WYDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYTVRTEHSLHEP	0; Mismatches 0; Indels 0;	99.7%; Score 1618; DB 4; Similarity 100.0%; Pred. No. 1.6e-137;	5271 MW;		EMBL: BC022401: AAH22401.1;	Submitted (FER-2002) to the EMBI/GenBank/DDBJ databases.	CTTOSUCE LUNG;	3	[1]	NCBI_TaxID=9606;	Catarrhini; Hominidae;	Craniata: Vertebrata:			(TrEMBLrel. 21, Creat		8TCB6 PRELIMINARY; PRT;	LT 1

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RESULT 3
Q8VBV9
ID Q8VBV9
AC Q8VBV9;
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Q8VGZ7
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Best Local Similarity
Matches 296; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang X., Firestein S.J.; "The olfactory receptor gene Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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nilarity 93.7%;
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Pred. No. 2.3e
9; Mismatches
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             PRT;
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Sciurognathi; Muridae;
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Best Local
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Q8VF09;
01-MAR-2002
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EMBL; A7073011; AAL60674.1; -.
EMBL; A7978854; AAL35109.1; -.
MGD; MG1:2157548; O1f1778.
InterPro; IPR000776; GPRC_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
Receptor.
SEQUENCE 320 AA; 35577 MW; 7161ACA8F4328959 CRO
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01-MAR-2002 (TrEMBLIE).
01-JUN-2002 (TrEMBLIE).
01factory receptor MORIE
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Zhang X., Firestein S.J.;
The olfactory receptor gene
Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
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OLFR78.
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AMFKIS
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8-2 (Prostate-specific G protein-coupled
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Pred. No. 5.3e-81;
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뭐 Ş 밁 Ş 밁 QΥ . 문 Ş 밁 Ş 밁 S

306

246

183

243

187

63

67

2

01-MAR-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.

Last Last

annotation update)

update)

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RESULT
Q8VH05
AC Q6
DT Q6
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                                                        01-MAR-2002 (TIEMBLIFEL 20, I

01-MAR-2002 (TIEMBLIFEL 20, I

01-JUN-2002 (TIEMBLIFEL 21, I

01factory receptor MOR10-1.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata;

Mammalla; Eutherla; Rodentla,

NCBI_TaxID=10090;
                                                                                                          Q8VH05;
Q8VH05;
01-MAR-2002;
01-MAR-2002;
01-JUN-2002;
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PROSITE;
PROSITE;
                   Zhang
*The c
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SEQUENCE
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 Nat.
[2]
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2002) to the EMBL; AY073732; AAL61395.1;
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      g X., Firestein S.J.; olfactory receptor gen Neurosci. 0:0-0(2002).
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                                                                                                                                                                                                                                                                                                                                                               AMAFDRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSH
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PS00339; AA_TRNA_LIGASE_II_2; UPS00337; G_PROTEIN_RECEP_F1_1; PS00237; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002106; AAtRNA_ligaseII.
IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322
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                                                                                                                                                   PRELIMINARY;
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Rodentia;
                                                                  Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.9%;
                   gene
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                                                                                                         Created)
Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 971.5; DB Pred. No. 2e-79;
                   superfamily
                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Sciurognathi; Muridae;
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                   mouse.";
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                                                                InterPro; IPR00276; GPCR_Rhodpsn.

Pfam; PF000130.; 'tm_1; 1.

PROSITE: PS000330. ''

PROSITE: PS000330. ''
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Best Local
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EMBL; AY072993; AAL50646.1; .
InterPro; IPR002106; AATRNA_ligaseII.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_l; 1.
PFAm; PF00001; 7tm_l; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Olfactory .... Mus musculus (Mouse).
Mus musculus (Mouse).
Mofazoa; Chordata;
                                                                                                                                                                                                                                                                                      Zhang X., Firestein S.J.; "The olfactory receptor gene Nat: Neurosci. 0:0-0(2002).
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                                     PROSITE; PS00339; AA_TRNA_LIGASE_II_2; PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
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169; Conservative
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312 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Rodentia;
34574 MW;
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Pred. No. 1.1e
64; Mismatches
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Last sequence update)
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                                                                                                                                                                                                EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; | Sciurognathi; Muridae;
CD233B37732052E5 CRC64;
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                                       UNKNOWN_1.
; UNKNOWN_1.
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; Murinae; Mus
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RESULT
Q8VGZ6
ID Q8VGZ6
AC Q8
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                                                                                                                                                                                                               Query Match
Best Local Sin
Matches 163;
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Best Local Similarity
Matches 165; Conserv
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01-MAR-2002 (TIEMBLIEL 20, I
01-JUN-2002 (TIEMBLIEL 21, I
01factory receptor MOR14-2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentla;
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                               PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY072994; AAL60657.1; -. InterPro; IPR002106; AATRNA_ligaseII. InterPro; IPR000276; GFCR_Rhodpsn.
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    123
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                                            62
                                                                                    63
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    FDRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYC
                                                              YIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMESTVLLAMA 122
                                                                                                                                                                     PNGNESSA--TYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g X., Firestein
olfactory recep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIRQRILRLF
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                                                                                                                               PSFNESTAYPPVFFLTGIPGLETSHTWISIPFCCLYAIAISGNSMILFVIITESSLHEPM
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                                                                                                                                                                                                                                                                                                                                    PF00001; 7tm_1; 1.
TE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
TE; PS00337; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
TE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                       314 AA;
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 estein S.J.;
y receptor gene :
. 0:0-0(2002).
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Rodentia;
                                                                                                                                                                                                                                                                                                       35096 MW;
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53.2%;
                                                                                                                                                                                                               54.2%; Score 879.5; DB 52.6%; Pred. No. 3.6e-71 tive 62; Mismatches 8
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                                                                                                                                                                                                                                                                                                       9F1016F881A040E9 CRC64;
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                                                                                                                                                                                                                                                          DB 11; Length
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Best Local Sin
Matches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M.;
Submitted (JAN-2002) to the EMBL/GenBank/TEMBL; AY072997; AAL60660.1; -.
EMBL; AY072997; AAL60660.1; -.
InterPro; IPR002106; AATRNA_1jgaseII.
InterPro; IPR00276; GPCR_Rhodpsn.
InterPro; IPR00276; GPCR_Rhodpsn.
Pf60001; 7tm_1; 1.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNP
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNP
PROSITE; PS00225; G_PROTEIN_RECEP_F1_2; 1.
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SEQUENCE
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-MAR-2002 (TrEMBLIel. 20,
01-JUN-2002 (TrEMBLIel. 21,
01factory receptor MOR10-2.
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                                                                                                                    CLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAF 240
                                                                                                                                                                                     AFDRYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKOLPFCRSNILSHSY 181
                                                                                                                                                                                                                                                                              RKAMLKVFFV
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                                                                                           CLHQDVMRLACASTRVNSLYGLIAVIFTKGSDSLSILISTVFILRTVMAIASGEGRLKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 54.7
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.1%; Score 877.5; DB
54.7%; Pred. No. 5.6e-71
Live 54; Mismatches 8
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Best Local Similarity
Matches 158; Conserv
              Q8VGZ2
Q8VGZ2;
Q8VGZ2;
Q1-MAR-2002 (TrEMBLrel. 20, C
Q1-MAR-2002 (TrEMBLrel. 20, L
Q1-JUN-2002 (TrEMBLrel. 21, L
Q1-JUN-2002 (TrEMBLrel. 21, L
Q1-GTORY receptor MOR30-1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VH17;
01-MAR-2002
01-MAR-2002
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY072971; AAL60634.1; -. IPR000276; GPCR_Rhodpsn. Ffam; pF00001; 7tm_1; 1. PF000175; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOW PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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Zhang X., Firestein
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    Eutheria;
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Rodentia;
Chordata;
Rodentia;
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Last annotation
                                                                           Created)
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Last annotation updat
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Sciurognathi; Muridae;
Craniata; Vertebrata; Sciurognathi; Muridae;
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    Euteleostomi;
; Murinae; Mus
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RESULT 11.
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Best Local S
Matches 155
           Submitted (JAN-2002) to the EMBL/GenB
EMBL, AY072987; AAL60650.1; -
InterPro; IPR002106; AAtRNA_11gaseII.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam, PF00001; 7tm_1; 1.
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"The olfactory receptor gen
Nat. Neurosci. 0:0-0(2002).
[2]
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Mammalia; Eutheria; Rodentia;
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01-MAR-2002 (TrEMBLIEL 20,
01-JUN-2002 (TrEMBLIEL 21,
01factory receptor MOR19-1.
                                                                                                                                                                                     Zhang X., Firestein S.J.;
"The olfactory receptor gene Nat. Neurosci. 0:0-0(2002).
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                                                                                                                           Adams M.;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
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                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Pred. No. 1.9e-70;
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                                                                                                                                                                                                             superfamily
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Best Local S
Matches 164
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Best Local Similarity
Matches 159; Conserv
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PROSITE;
PROSITE;
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SEQUENCE
                                                                                              SEQUENCE FROM N.A.
Zhang X., Firestein S.J.;
The olfactory receptor gene
Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                    01-MAR-2002 (TIEMBLIEL 20,
01-MAR-2002 (TIEMBLIEL 20,
01-JUN-2002 (TIEMBLIEL 21,
01factory receptor MOR17-2.
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Q8VGZ8;
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                                                                                                                                                                                                                                                                                                          VPFIGLSMYHRESKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHV
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                                                              Similarity
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PS00237;
PS50262;
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G_PROTEIN_RECEP_F1_1;
G_PROTEIN_RECEP_F1_2;
                                                                                   36040 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.4%;
                                                       53.1%; Score 861.5;
53.2%; Pred. No. 1.50
Live 56; Mismatches
                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 866.5; L
Pred. No. 5.4e-
58; Mismatches
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Last annotation update)
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Sciurognathi; Muridae;
                                                                                   D3FF22D8755FDC2F CRC64;
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No. 5.4e-70;
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les 87;
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; Murinae; Mus
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Best Local Similarity
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01-MAR-2002 (TIEMBLIEL 20,
01-JUN-2002 (TIEMBLIEL 21,
01factory receptor MOR28-1.
                                                                                                                                                                                                                                          Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY072984; AAL60647.1; -
InterPro; IPR000276; GPCC_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Zhang X., Firestein S.J.;
Than olfactory receptor gene
Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                               Q8VH04
                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                          PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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 RILRLF 309
                                                                               RYVAICKPLHYTTILTKPLIIKIGLAAVTRAVTLMTPLPFLLRRFHYCRGTVIAHCYCEH
                                                                                      RYVAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLH
                                                                                                                              FLCMLSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQMFAIHSLSGMESTVLLAMAFD 124
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                                                                                                                                                                                                           35851 MW;
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Last sequence update)
Last annotation update)
                                                                                                                                                                            Score 858; DB 11; Length 317; Pred. No. 3.1e-69; B; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                        superfamily
                                                                                                                                                                                                           A7ABD897C708D04B CRC64;
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Best Local S
Matches 154
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SEQUENCE
                 Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
NOR 3'Beta4 (Olfactory receptor MOR17-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY073034; AAL60697.1; -
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                 Q9EQQ7;
                                                                                           09EQQ7
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"The olfactory receptor gene Nat. Neurosci. 0:0-0(2002).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8VGW0
 NCBI_TaxID-10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                       prosite; ps00237; G_protein_recep_r1_1;
prosite; ps50262; G_protein_recep_f1_2;
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                           PRELIMINARY;
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Rodentia;
                   Rodentia;
                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                       35988 MW;
                                                                                                                                                                                                                                                                                                                                                                 52.8%; Score 857.5; DB 11
49.4%; Pred. No. 3.5e-69;
Live 67; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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                  Craniata; Vertebrata;
Sciurognathi; Muridae;
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                   Muridae;
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; Murinae; Mus
                            Euteleostomi;
                   Murinae;
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                    Mus
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Matches
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Best Local Similarity
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SEQUENCE
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Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell (
Felsenfeld G., Groudine M., Hardison R.;
"Comparative structural and functional analysis of the olfactory
receptor genes flanking the human and mouse beta -globin gene
clusters.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AF133300; AAG41684.1; -. EMBL; AY072988; AAL60651.1; -. Interpro; IPR000276; GPCR_Rhodpsn.
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                                  IRQRILRL
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                                                                                                                                              CLHQDMIRLACADIRFNVIYGLVLITLLWGMDSLGIFVSYVLILHSVLKIASREGRLKAL
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IREGILHL
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308
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Pred. No. 4.3e-69;
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